C.   establishing a distribution set of probability distributions, including at least one

        distribution, associating hypothetical reaction values with corresponding

        probabilities for each genotype of interest at the locus;

D.   applying the first reaction value to each pertinent probability distribution to

        determine a measure of a conditional probability of each genotype of

        interest at the locus; and

E.   determining the genotype based on the data obtained from step (D).

76.   (New) A method according to claim 75, wherein the distribution set includes a

plurality of probability distributions for a corresponding plurality of genotypes of interest.

77.   (New) A method, according to claim 75, further comprising:

        (i)   reacting the material at the locus to produce a second reaction

                value independently indicative of the presence of a second allele

                at the locus;

        (ii)   forming a second data set including the second reaction value; and

        (iii)   applying the first and second reaction values to each pertinent

                distribution to determine a measure of the conditional probability

                of each genotype at the locus.

29302.1

78. (New) A method according to claim 76, further comprising:

    (i)   reacting the material at the locus to produce a second reaction value;

    (ii)   applying the first and second reaction values to each pertinent distribution to determine the probability of each genotype at the locus; and

    (iii) applying the first and second reaction values to each pertinent distribution to determine a measure of the conditional probability of each genotype at the locus.

79. (New) A method according to claim 77, wherein each probability distribution associates a hypothetical pair of first and second reaction values with a single probability of each genotype of interest.

80. (New) A method according to claim 75, wherein:

    step (B) includes the step of including in the data set other reaction values obtained under conditions comparable to those under which the first reaction value was produced; and

    step (C) includes the step of using the reaction values in the data set to establish the probability distributions;

the method further comprising:

performing steps (D) and (E) with respect to each of the reaction values.

81.   (New) A method, according to claim 80, of determining the genotype at a locus within genetic material obtained from each of a plurality of samples, the method further comprising:

(i)   performing step (A) with respect to the locus of material obtained from each sample;

(ii)   in step (B), including in the data set reaction values obtained from each sample.

D'
Cout.

82.   (New) A method according to claim 80, of determining the genotype of selected loci within genetic material obtained from a sample, the method further comprising:

(i)   performing step (A) at each of the selected loci;

(ii)   in step (B), including in the data set reaction values obtained from each of the selected loci.

83. (New) A method according to claim 80, wherein step (C) includes:

(i) establishing a set of initial probability distributions that associate hypothetical reaction values with corresponding probabilities for each genotype of interest at the locus;

(ii) using the initial probability distributions to determine measures of the initial conditional probability for each genotype at the locus; and

(iii) using the results of step (ii) to modify the initial probability distributions, so that the modified distributions more accurately reflect the reaction values in the data set.

84. (New) A method according to claim 83, wherein step (C) further includes:

(iv) repeating steps (i) through (iii) a desired number of times.

85. (New) A method according to claim 75, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data obtained from step (D).

86. (New) A method according to claim 80, wherein step (E) further includes the step of calculating a confidence score, associated with the genotype being determined, based on data from step (D), the method further comprising:

29302.1

(F) determining whether a significant downward trend in confidence scores has occurred, and, in such event, entering an alarm condition.

87. (New) A method according to claim 75, wherein each allele is a single specific nucleotide.

88. (New) A method according to claim 75, wherein each allele consists of at least two specific nucleotides.

89. (New) A method according to claim 75, wherein each allele is defined at least in part by its length in nucleotides.

90. (New) A method according to claim 75, wherein each allele is defined by one of the presence and absence of at least one restriction site.

91. (New) A method according to claim 78, wherein step (B) includes the step of including in the data set reaction values from prior tests at the locus obtained under comparable conditions.

29302.1